Molecular Analysis Tools Knowledge Center

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Welcome!

The caBIG® Molecular Analysis Tools Knowledge Center (MATKC) is an NCI-supported entity led by the Columbia University Herbert Irving Comprehensive Cancer Center with The Broad Institute of MIT and Harvard. The Knowledge Center provides a centralized, authoritative repository of knowledge, information, and web-based support to facilitate the deployment and ongoing development of caBIG® tools, standards, and infrastructure in the molecular analysis domain. Key services provided by the Knowledge Center include:

- Providing domain expertise on using the supported tools to carry out molecular analysis
- Posting up-to-date installation packages for related tools
- Maintaining technical and end-user documentation
- Fostering open source development of caBIG® tools by the community
- Collecting and monitoring defect reports, feature requests, and end-user requirements

For First-time Visitors

If you want to post in the forum or add entries into the defect tracking/feature request system, please create a free account at KC signup.

Upon receiving your account credentials, you can post messages to the forums. To receive email notification when responses to your posts are made, simply click the "subscribe forum" or "subscribe topic" link at the bottom of the page.

If you have been using various email lists for the tools below, please be advised that forums hosted by this knowledge center will gradually become the main vehicle for your comments and questions on the tools. The email lists will be used mainly for announcements in the near future. Thank you for your understanding and support. Please let us know you thoughts and experience with this new channel of communication so that we can make it better.

What's New

Most recent Software Releases

- caArray 2.4.1 was released on 10/3/2011
- geWorkbench 2.2.2 was released on 8/19/2011
- caIntegrator 1.3 was released on 6/17/2011
- GenePattern 3.3.2 was released on 6/2011
- caGWAS 1.1.0 was released on 11/6/2009

For more news, visit What's New.

Tools Supported by the MAT KC

The following software tools are currently supported by the Molecular Analysis Tools Knowledge Center. Links are provided to the tool summary page for each tool, which provides an overview of the tool with links to resources including the knowledge base, forum, bug tracker, feature request system, and the developer's code repository.

caArray

caArray is an open-source microarray data management system which is accessible both via the web and programmatically. caArray guides the annotation and exchange of array data using a federated model of local installations whose results are shareable across the cancer Biomedical Informatics Grid (caBIG®). Visit the caArray page for more information.

caIntegrator

caIntegrator is a web-based software application that allows researchers to set up custom, caBIG®-compatible web portals to conduct integrative research, without requiring programming experience. These portals bring together heterogeneous clinical, microarray and medical imaging data to enrich multidisciplinary research. Visit the caIntegrator page for more information.

geWorkbench

geWorkbench (genomics Workbench) is a Java-based open-source platform for integrated genomics. Using a component architecture it allows individually developed plug-ins to be configured into complex bioinformatic applications. At present there are more than 50 available plug-ins supporting the visualization and analysis of gene expression and sequence data. Visit the geWorkbench page for more information.

GenePattern

GenePattern combines a powerful scientific workflow platform with more than 150 computational and visualization tools for the analysis of genomic data. Visit the GenePattern page for more information.

Tool Adoption Case Studies

Many academic institutes and research/commercial organizations have adopted various caBIG tools in the past. In this section we link to a few key documents where caBIG tool adopters have created materials about their experience for the benefit of those considering an adoption project of their own.

From the Jackson Laboratory:

ICR Tools Aoption Project Outcome Presentation

Lessons Learned Presentation

Integration of Tools

There is extensive integration among caArray, caIntegrator2, caIntegrator, geWorkbench, and GenePattern. For example, geWorkbench and caIntegrator2 can retrieve microarray data directly from caArray hosted at NCI or on a local server. GenePattern is also connected to caArray for data retrieval. caIntegrator2 and caIntegrator use GenePattern as one of its data analysis services.

Instead of developing all data analysis modules independently, geWorkbench and GenePattern each can invoke several modules of the other party to provide a comprehensive data analysis platform. To learn how to use these tools together, please check out corresponding tool's wiki pages as well as the forums (End Users forum and Developers forum) dedicated to the integration of these tools.

Visit MAT Knowledge Center Forum

The Molecular Analysis Tools Domain Forum. is for visitors to submit questions and comments that are beyond the scope of any specific tool, but that are within the domain addressed by the Knowledge Center. What questions or comments do you have that extend beyond the coverage of the existing caBIG® tool set? Write your thoughts in this forum, so that they can be answered by the Knowledge Center Team and/or brought to appropriate stakeholder groups such as the Integrative Cancer Research (ICR) workspace.

Related Links

- ICR Workspace (On caBIG® Community Website)
- Support Service Provider Listing
- caBIG® Community Website